

1

## SEQUENCE LISTING

&lt;110&gt; AXXAM SRL

&lt;120&gt; photoproteins with enhanced bioluminescence and assays using the same

&lt;130&gt; 1489EUR

&lt;160&gt; 22

&lt;170&gt; PatentIn version 3.1

&lt;210&gt; 1

&lt;211&gt; 198

&lt;212&gt; PRT

&lt;213&gt; Clytia gregaria

&lt;400&gt; 1

Met Ala Asp Thr Ala Ser Lys Tyr Ala Val Lys Leu Arg Pro Asn Phe  
1 5 10 15

Asp Asn Pro Lys Trp Val Asn Arg His Lys Phe Met Phe Asn Phe Leu  
20 25 30

Asp Ile Asn Gly Asp Gly Lys Ile Thr Leu Asp Glu Ile Val Ser Lys  
35 40 45

Ala Ser Asp Asp Ile Cys Ala Lys Leu Gly Ala Thr Pro Glu Gln Thr  
50 55 60

Lys Arg His Gln Asp Ala Val Glu Ala Phe Phe Lys Lys Ile Gly Met  
65 70 75 80

Asp Tyr Gly Lys Glu Val Glu Phe Pro Ala Phe Val Asp Gly Trp Lys  
85 90 95

Glu Leu Ala Asn Tyr Asp Leu Lys Leu Trp Ser Gln Asn Lys Lys Ser  
100 105 110

2

Leu Ile Arg Asp Trp Gly Glu Ala Val Phe Asp Ile Phe Asp Lys Asp  
115 120 125

Gly Ser Gly Ser Ile Ser Leu Asp Glu Trp Lys Ala Tyr Gly Arg Ile  
130 135 140

Ser Gly Ile Cys Ser Ser Asp Glu Asp Ala Glu Lys Thr Phe Lys His  
145 150 155 160

Cys Asp Leu Asp Asn Ser Gly Lys Leu Asp Val Asp Glu Met Thr Arg  
165 170 175

Gln His Leu Gly Phe Trp Tyr Thr Leu Asp Pro Asn Ala Asp Gly Leu  
180 185 190

Tyr Gly Asn Phe Val Pro  
195

<210> 2

<211> 198

<212> PRT

<213> Unknown

<220>

<223> Clytin mutant: mutClyK1

<400> 2

Met Ala Asp Thr Ala Ser Lys Tyr Ala Val Lys Leu Arg Pro Asn Phe  
1 5 10 15

Asp Asn Pro Lys Trp Val Asn Arg His Lys Phe Met Phe Asn Phe Leu  
20 25 30

Asp Ile Asn Gly Asp Gly Lys Ile Thr Leu Asp Glu Ile Val Ser Lys  
35 40 45

Ala Ser Asp Asp Ile Ser Ala Lys Leu Gly Ala Thr Pro Glu Gln Thr  
50 55 60

Lys Arg His Gln Asp Ala Val Glu Ala Phe Phe Lys Lys Ile Gly Met  
65 70 75 80

Asp Tyr Gly Lys Glu Val Glu Phe Pro Ala Phe Val Asp Gly Trp Lys  
85 90 95

3

Glu Leu Ala Asn Tyr Asp Leu Lys Leu Trp Ser Gln Asn Lys Lys Ser  
100 105 110

Leu Ile Arg Asp Trp Gly Glu Ala Val Phe Asp Ile Phe Asp Lys Asp  
115 120 125

Gly Ser Gly Ser Ile Ser Leu Asp Glu Trp Lys Ala Tyr Gly Arg Ile  
130 135 140

Ser Gly Ile Cys Ser Ser Asp Glu Asp Ala Glu Lys Thr Phe Lys His  
145 150 155 160

Cys Asp Leu Asp Asn Ser Gly Lys Leu Asp Val Asp Glu Met Thr Arg  
165 170 175

Gln His Leu Gly Phe Trp Tyr Thr Leu Asp Pro Asn Ala Asp Gly Leu  
180 185 190

Tyr Gly Asn Phe Val Pro  
195

&lt;210&gt; 3

&lt;211&gt; 198

&lt;212&gt; PRT

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; Clytin mutant: mutClyK4

&lt;400&gt; 3

Met Ala Asp Thr Ala Ser Lys Tyr Ala Val Lys Leu Arg Pro Asn Phe  
1 5 10 15

Asp Asn Pro Lys Trp Val Asn Arg His Lys Phe Met Phe Asn Phe Leu  
20 25 30

Asp Ile Asn Gly Asp Gly Lys Ile Thr Leu Asp Glu Ile Val Ser Lys  
35 40 45

Ala Ser Asp Asp Ile Cys Ala Lys Leu Gly Ala Thr Pro Glu Gln Thr  
50 55 60

Lys Arg His Gln Asp Ala Val Glu Ala Phe Phe Lys Lys Ile Gly Met  
65 70 75 80

4

Asp Tyr Gly Lys Glu Val Glu Phe Pro Ala Phe Val Asp Gly Trp Lys  
85 90 95

Glu Leu Ala Asn Tyr Asp Leu Lys Leu Trp Ser Gln Asn Lys Lys Ser  
100 105 110

Leu Ile Arg Asp Trp Gly Glu Ala Val Phe Asp Ile Phe Asp Lys Asp  
115 120 125

Gly Ser Gly Cys Ile Ser Leu Asp Glu Trp Lys Ala Tyr Gly Arg Ile  
130 135 140

Ser Gly Ile Cys Ser Ser Asp Glu Asp Ala Glu Lys Thr Phe Lys His  
145 150 155 160

Cys Asp Leu Asp Asn Ser Gly Lys Leu Asp Val Asp Glu Met Thr Arg  
165 170 175

Gln His Leu Gly Phe Trp Tyr Thr Leu Asp Pro Asn Ala Asp Gly Leu  
180 185 190

Tyr Gly Asn Phe Val Pro  
195

&lt;210&gt; 4

&lt;211&gt; 198

&lt;212&gt; PRT

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; Clytin mutant: 1F10 mutant

&lt;400&gt; 4

Met Ala Asp Thr Ala Ser Lys Tyr Ala Val Lys Leu Arg Pro Asn Phe  
1 5 10 15

Asp Asn Pro Lys Trp Val Asn Arg His Lys Phe Met Phe Asn Phe Leu  
20 25 30

Asp Ile Asn Gly Asp Gly Lys Ile Thr Leu Asp Glu Ile Val Ser Arg  
35 40 45

Ala Ser Asp Asp Ile Cys Ala Lys Leu Gly Ala Thr Pro Glu Gln Thr  
50 55 60

5

Lys Arg His Gln Asp Ala Val Glu Ala Phe Phe Lys Lys Ile Gly Met  
65 70 75 80

Asp Tyr Gly Lys Glu Val Glu Phe Pro Ala Phe Val Asp Gly Trp Lys  
85 90 95

Glu Leu Ala Asn Tyr Asp Leu Lys Leu Trp Ser Gln Asn Lys Lys Ser  
100 105 110

Leu Ile Arg Asp Trp Gly Glu Ala Val Phe Asp Ile Phe Asp Lys Asp  
115 120 125

Gly Ser Gly Ser Ile Ser Leu Asp Glu Trp Lys Ala Tyr Gly Arg Ile  
130 135 140

Ser Gly Ile Cys Ser Ser Asp Glu Asp Ala Glu Lys Thr Phe Lys His  
145 150 155 160

Cys Asp Leu Asp Asn Ser Gly Lys Leu Asp Val Asp Glu Met Thr Arg  
165 170 175

Gln His Leu Gly Phe Trp Tyr Thr Leu Asp Pro Asn Ala Asp Gly Leu  
180 185 190

Tyr Gly Asp Phe Val Pro  
195

<210> 5

<211> 198

<212> PRT

<213> Unknown

<220>

<223> Clytin mutant: 1H7 mutant

<400> 5

Met Ala Asp Thr Ala Ser Lys Tyr Ala Val Lys Leu Arg Pro Asn Phe  
1 5 10 15

Asp Asn Pro Lys Trp Val Asn Arg His Lys Phe Met Phe Asn Phe Leu  
20 25 30

Asp Ile Asn Gly Asp Gly Lys Ile Thr Leu Asp Glu Ile Val Ser Lys  
35 40 45

6

Ala Ser Asp Asp Ile Cys Ala Lys Leu Gly Ala Thr Pro Glu Gln Thr  
50 55 60

Lys Arg His Arg Asp Ala Val Glu Ala Phe Phe Lys Lys Ile Gly Met  
65 70 75 80

Asp Tyr Gly Lys Glu Val Glu Phe Pro Val Phe Val Asp Gly Trp Lys  
85 90 95

Glu Leu Ala Asn Tyr Asp Leu Lys Leu Trp Ser Gln Asn Lys Lys Ser  
100 105 110

Leu Ile Arg Asp Trp Gly Glu Ala Val Phe Asp Ile Phe Asp Lys Asp  
115 120 125

Gly Ser Gly Ser Ile Ser Leu Asp Glu Trp Lys Ala Tyr Gly Arg Ile  
130 135 140

Ser Gly Ile Cys Ser Ser Asp Glu Asp Ala Glu Lys Thr Phe Lys His  
145 150 155 160

Cys Asp Leu Asp Asn Ser Gly Lys Leu Asp Val Asp Glu Met Thr Arg  
165 170 175

Gln His Leu Gly Phe Trp Tyr Ile Leu Asp Pro Asn Ala Asp Gly Leu  
180 185 190

Tyr Gly Asn Phe Val Pro  
195

<210> 6

<211> 198

<212> PRT

<213> Unknown

<220>

<223> Clytin mutant: 1C12 mutant

<400> 6

Met Ala Asp Thr Ala Ser Lys Tyr Ala Val Lys Leu Arg Pro Asn Phe  
1 5 10 15

Asp Asn Pro Lys Trp Val Asn Arg His Lys Phe Met Phe Asn Phe Leu  
20 25 30

7

Asp Ile Asn Gly Asp Gly Lys Ile Thr Leu Asp Glu Ile Val Ser Lys  
35 40 45

Ala Ser Asp Asp Ile Cys Ala Lys Leu Gly Ala Thr Pro Glu Gln Thr  
50 55 60

Lys Arg His Gln Asp Ala Val Glu Ala Phe Phe Lys Lys Ile Gly Met  
65 70 75 80

Asp Phe Gly Lys Glu Val Glu Phe Pro Ala Phe Val Asp Gly Trp Lys  
85 90 95

Glu Leu Ala Asn Tyr Asp Leu Lys Leu Trp Ser Gln Asn Asn Lys Ser  
100 105 110

Leu Ile Arg Asp Trp Gly Glu Ala Val Phe Asp Ile Leu Asp Lys Asp  
115 120 125

Gly Ser Gly Ser Ile Ser Leu Asp Glu Trp Lys Ala Tyr Gly Arg Ile  
130 135 140

Ser Gly Ile Cys Arg Ser Asp Glu Asp Ala Glu Lys Thr Phe Lys His  
145 150 155 160

Cys Asp Leu Asp Asn Ser Gly Lys Leu Asp Val Asp Glu Met Thr Arg  
165 170 175

Gln His Leu Gly Phe Trp Tyr Thr Leu Asp Pro Asn Ala Asp Gly Leu  
180 185 190

Tyr Gly Asn Phe Val Pro  
195

<210> 7

<211> 198

<212> PRT

<213> Unknown

<220>

<223> Clytin mutant: 25N03b mutant

<400> 7

Met Ala Asp Thr Ala Ser Lys Tyr Ala Val Lys Leu Arg Pro Asn Phe  
1 5 10 15

8

Asp Asn Pro Lys Trp Val Asn Arg His Lys Phe Met Phe Asn Phe Leu  
20 25 30

Asp Ile Asn Gly Asp Gly Lys Ile Thr Leu Asp Glu Ile Val Ser Lys  
35 40 45

Ala Ser Asp Asp Ile Cys Ala Lys Leu Gly Ala Thr Pro Glu Gln Thr  
50 55 60

Lys Arg His Gln Asp Ala Val Glu Ala Phe Phe Lys Lys Ile Gly Met  
65 70 75 80

Asp Tyr Gly Lys Glu Val Glu Phe Pro Ala Phe Val Asp Gly Trp Lys  
85 90 95

Glu Leu Ala Asn Tyr Asp Leu Lys Leu Trp Ser Gln Asn Lys Lys Ser  
100 105 110

Leu Ile Arg Asp Trp Gly Glu Ala Val Phe Asp Ile Phe Asp Lys Asp  
115 120 125

Gly Ser Gly Ser Ile Ser Leu Asp Glu Trp Lys Ala Tyr Cys Arg Ile  
130 135 140

Ser Gly Ile Cys Ser Ser Asp Glu Asp Ala Glu Lys Thr Phe Lys His  
145 150 155 160

Cys Asp Leu Asp Asn Ser Gly Lys Leu Asp Val Asp Glu Met Thr Arg  
165 170 175

Gln His Leu Gly Phe Trp Tyr Thr Leu Asp Pro Asn Ala Asp Gly Leu  
180 185 190

Tyr Gly Asn Phe Val Pro  
195

<210> 8

<211> 198

<212> PRT

<213> Unknown

<220>

<223> Clytin mutant: 3C12 mutant



9

&lt;400&gt; 8

Met Ala Asp Thr Ala Ser Lys Tyr Ala Val Lys Leu Arg Pro Asn Phe  
1 5 10 15

Asp Asn Pro Lys Trp Val Asn Arg His Lys Phe Met Phe Asn Phe Leu  
20 25 30

Asp Ile Asn Gly Asp Gly Lys Ile Thr Leu Asp Glu Ile Val Ser Lys  
35 40 45

Ala Ser Asp Asp Val Cys Ala Lys Leu Gly Ala Thr Pro Glu Gln Thr  
50 55 60

Lys Arg His Gln Asp Ala Val Glu Ala Phe Phe Lys Lys Ile Gly Met  
65 70 75 80

Asp Tyr Gly Lys Glu Val Glu Phe Pro Ala Phe Val Asp Gly Trp Lys  
85 90 95

Glu Leu Ala Asn Tyr Asp Leu Lys Leu Trp Ser Gln Asn Lys Lys Ser  
100 105 110

Leu Ile Arg Asp Trp Gly Glu Ala Val Phe Asp Ile Phe Asp Lys Asp  
115 120 125

Gly Ser Gly Ser Ile Ser Leu Asp Glu Trp Lys Ala Tyr Gly Arg Ile  
130 135 140

Ser Gly Ile Cys Arg Ser Asp Glu Asp Ala Glu Lys Thr Phe Lys His  
145 150 155 160

Cys Asp Leu Asp Asn Ser Gly Lys Leu Asp Val Asp Glu Met Thr Arg  
165 170 175

Gln His Leu Gly Phe Trp Tyr Thr Leu Asp Pro Asn Ala Asp Gly Leu  
180 185 190

Tyr Gly Asn Phe Val Pro  
195

&lt;210&gt; 9

&lt;211&gt; 198

&lt;212&gt; PRT

&lt;213&gt; Unknown

10

&lt;220&gt;

&lt;223&gt; Clytin mutant: 6H22 mutant

&lt;400&gt; 9

Met Ala Asp Thr Ala Ser Lys Tyr Ala Val Lys Leu Arg Pro Asn Phe  
1 5 10 15

Asp Asp Pro Lys Trp Val Asn Arg His Lys Phe Met Phe Asn Phe Leu  
20 25 30

Asp Ile Asn Gly Asp Gly Lys Val Thr Leu Asp Glu Ile Val Ser Lys  
35 40 45

Ala Ser Asp Asp Ile Cys Ala Arg Leu Gly Ala Thr Pro Glu Gln Thr  
50 55 60

Lys Arg His Gln Asp Ala Val Glu Ala Phe Phe Lys Lys Ile Gly Met  
65 70 75 80

Asp Tyr Gly Lys Glu Val Glu Phe Pro Ala Phe Val Asp Gly Trp Lys  
85 90 95

Glu Leu Ala Asn Tyr Asp Leu Lys Leu Trp Ser Gln Asn Lys Lys Ser  
100 105 110

Leu Ile Arg Asp Trp Gly Glu Ala Val Phe Asp Ile Phe Asp Lys Asp  
115 120 125

Gly Ser Gly Ser Ile Ser Leu Asp Glu Trp Lys Ala Tyr Gly Arg Ile  
130 135 140

Ser Gly Ile Cys Ser Ser Asp Glu Asp Ala Glu Lys Thr Phe Lys His  
145 150 155 160

Cys Asp Leu Asp Asn Ser Gly Lys Leu Asp Val Asp Glu Met Thr Arg  
165 170 175

Gln His Leu Gly Phe Trp Tyr Thr Leu Asp Pro Asn Ala Asp Gly Leu  
180 185 190

Tyr Gly Asn Phe Val Pro  
195

&lt;210&gt; 10

&lt;211&gt; 198

11

&lt;212&gt; PRT

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; Clytin mutant: 12mutCly

&lt;400&gt; 10

Met Ala Asp Thr Ala Ser Lys Tyr Ala Val Lys Leu Arg Pro Asn Phe  
1 5 10 15

Asp Asn Pro Lys Trp Val Asn Arg His Lys Phe Met Phe Asn Phe Leu  
20 25 30

Asp Ile Asn Gly Asp Gly Lys Ile Thr Leu Asp Glu Ile Val Ser Lys  
35 40 45

Ala Ser Asp Asp Ile Cys Ala Lys Leu Glu Ala Thr Pro Glu Gln Thr  
50 55 60

Lys Arg His Gln Val Cys Val Glu Ala Phe Phe Arg Gly Cys Gly Met  
65 70 75 80

Glu Tyr Gly Lys Glu Ile Ala Phe Pro Gln Phe Leu Asp Gly Trp Lys  
85 90 95

Gln Leu Ala Thr Ser Glu Leu Lys Lys Trp Ala Arg Asn Glu Pro Thr  
100 105 110

Leu Ile Arg Glu Trp Gly Asp Ala Val Phe Asp Ile Phe Asp Lys Asp  
115 120 125

Gly Ser Gly Ser Ile Ser Leu Asp Glu Trp Lys Ala Tyr Gly Arg Ile  
130 135 140

Ser Gly Ile Cys Ser Ser Asp Glu Asp Ala Glu Lys Thr Phe Lys His  
145 150 155 160

Cys Asp Leu Asp Asn Ser Gly Lys Leu Asp Val Asp Glu Met Thr Arg  
165 170 175

Gln His Leu Gly Phe Trp Tyr Thr Leu Asp Pro Asn Ala Asp Gly Leu  
180 185 190

Tyr Gly Asn Phe Val Pro  
195

12

&lt;210&gt; 11

&lt;211&gt; 600

&lt;212&gt; DNA

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; Clytin mutant: mutClyK1\_dna

&lt;400&gt; 11

atggccgaca ccgccagcaa gtacgccgtg aagctgaggc ccaacttoga caaccccaag 60

tgggtgaacc ggcacaagtt catgttcaac ttcttgga tcaacggcga cggcaagatc 120

accctggacg agatcgtgag caaggccagc gacgacatct gcgccaaagct gggcgccacc 180

cccagacaga ccaagagaca ccaggacgoc gtggaggcct tcttcaagaa gatcggcatg 240

gactacggca aggaggtgga gttccccgcc ttcgtggacg gctggaagga gctggccaac 300

taccacctga agctgtggag ccagaacaag aagagcctca tcagggactg gggcgaggcc 360

gtgttcgaca tcttcgacaa ggacggcagc ggctgcatca gcctggatga gtggaaggcc 420

tacggcagaa tcagcggcat ctgcagcagc gacgaggacg ccgaaaagac cttcaagcac 480

tgcgacctgg acaacagcgg caagctggac gtggacgaga tgaccagaca gcacctggac 540

ttctggtaaa ccttggaccc caatgccgac ggctgtacg gcaacttcgt gccttgataa 600

&lt;210&gt; 12

&lt;211&gt; 600

&lt;212&gt; DNA

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; Clytin mutant: mutClyK4\_dna

&lt;400&gt; 12

atggccgaca ccgccagcaa gtacgccgtg aagctgaggc ccaacttoga caaccccaag 60

tgggtgaacc ggcacaagtt catgttcaac ttcttgga tcaacggcga cggcaagatc 120

accctggacg agatcgtgag caaggccagc gacgacatct gcgccaaagct gggcgccacc 180

cccagacaga ccaagagaca ccaggacgoc gtggaggcct tcttcaagaa gatcggcatg 240

gactacggca aggaggtgga gttccccgcc ttcgtggacg gctggaagga gctggccaac 300

tacgacctga agctgtggag ccagaacaag aagagcctca tcagggactg gggcgaggcc 360

## 13

gtgttcgaca tcttcgacaa ggacggcagc ggctgcatca gcctggatga gtggaaggcc 420  
tacggcagaa tcagcggcat ctgcagcagc gacgaggacg ccgaaaagac cttcaagcac 480  
tgcgacctgg acaacagcgg caagctggac gtggacgaga tgaccagaca gcacctgggc 540  
ttctggtaca ccctggaccc caatgccgac ggctgtacg gcaacttcgt gccttgataa 600

&lt;210&gt; 13

&lt;211&gt; 600

&lt;212&gt; DNA

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; Clytin mutant: 1F10 mutant\_dna

&lt;400&gt; 13

atggccgaca ccgccagcaa gtacgccgtg aagctgaggc ccaacttcga caaccccaag 60  
tgggtgaacc ggcacaagtt catgttcaac ttcttgga tcaacggcga cggcaagatc 120  
accctggacg agatcgtgag cagggccagc gacgacatct gcgccaaagt gggcgccacc 180  
cccgagcaga ccaagagaca ccaggacgcc gtggaggcct tcttcaagaa gatcggcatg 240  
gactacggca aggaggtgga gttccccgcc ttcgtggacg gctggaagga gctggccaac 300  
tacgacctga agctgtggag ccagaacaag aagagcctca tcagggactg gggcgaggcc 360  
gtgttcgaca tcttcgacaa ggacggcagc ggcagcatca gcctggatga gtggaaggcc 420  
tacggcagaa tcagcggcat ctgcagcagc gacgaggacg ccgaaaagac cttcaagcac 480  
tgcgacctgg acaacagcgg caagctggac gtggacgaga tgaccagaca gcacctgggc 540  
ttctggtaca ccctggaccc caacgccgac ggctgtacg gcgacttcgt gccttgataa 600

&lt;210&gt; 14

&lt;211&gt; 600

&lt;212&gt; DNA

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; Clytin mutant: 1H7 mutant\_dna

&lt;400&gt; 14

atggccgaca ccgccagcaa gtacgccgtg aagctgaggc ccaacttcga caaccccaag 60

14

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| tgggtgaacc  | ggcacaagtt | catgttcaat | ttcctggaca | tcaacggcga | cggcaagatc | 120 |
| accctggacg  | agatcgtgag | caaggccagc | gacgacatct | gcgccaagct | gggcgccacc | 180 |
| cccagagcaga | ccaagagaca | ccgggacgcc | gtggaggcct | tcttcaagaa | gatcggcatg | 240 |
| gactacggca  | aggaggtgga | gttccccgtc | ttcgtggacg | gctggaagga | gctggccaac | 300 |
| tacgacctga  | agctgtggag | ccagaacaag | aagagcctca | tcagggactg | gggcgaggcc | 360 |
| gtgtttgaca  | tcttcgacaa | ggacggcagc | ggcagcatta | gcctggatga | gtggaaggcc | 420 |
| tacggtagaa  | tcagcggcat | ctgcagcagc | gacgaggacg | ccgaaaagac | cttcaagcac | 480 |
| tgcgacctgg  | acaacagcgg | caagctggac | gtggacgaga | tgaccagaca | gcacctgggc | 540 |
| ttctggtaca  | tcctggaccc | caacgccgac | ggcctgtacg | gcaacttcgt | gccttgataa | 600 |

<210> 15

<211> 600

<212> DNA

<213> Unknown

<220>

<223> Clytin mutant: 1C12 mutant\_dna

<400> 15

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| atggccgaca  | ccgccagcaa | gtacgccgtg | aagctgaggg | ccaacttcga | caaccccaag | 60  |
| tgggtgaacc  | ggcacaagtt | catgttcaac | ttcctggaca | tcaacggcga | cggcaagatc | 120 |
| accctggacg  | agatcgtgag | caaggccagc | gacgacatct | gcgccaagct | gggcgccacc | 180 |
| cccagagcaga | ccaagagaca | ccaggacgcc | gtggaggcct | tcttcaagaa | gatcggcatg | 240 |
| gacttcggca  | aggaggtgga | gttccccgcc | ttcgtggacg | gctggaagga | gctggccaac | 300 |
| tacgacctga  | agctgtggag | ccagaacaat | aagagcctca | tcagggactg | gggcgaggcc | 360 |
| gtgttcgaca  | tcctcgacaa | ggacggcagc | ggcagcatca | gcctggatga | gtggaaggcc | 420 |
| tacggcagaa  | tcagcggcat | ctgcagaagc | gacgaggacg | ccgaaaagac | cttcaagcac | 480 |
| tgcgacctgg  | acaacagcgg | caagctggac | gtggacgaga | tgaccagaca | gcacctgggc | 540 |
| ttctggtaca  | ccctggaccc | caacgccgac | ggcctgtacg | gcaacttcgt | gccttgataa | 600 |

<210> 16

<211> 600

<212> DNA

15

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; Clytin mutant: 25N03b mutant\_dna

&lt;400&gt; 16

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| atggccgaca | ccgccagcaa | gtacgccgtg | aagctgaggc | ccaacttcga | caaccccaag | 60  |
| tgggtgaacc | ggcacaagtt | catgttcaac | ttcctggaca | tcaacggcga | cggcaagatc | 120 |
| accctggacg | agatcgtgag | caaggccagc | gacgacatct | gcgccaagct | gggcgccacc | 180 |
| cccgagcaga | ccaagagaca | ccaggacgcc | gtggaggcct | tcttcaagaa | gatcggcatg | 240 |
| gactacggca | aggaggtgga | gttccccgcc | ttcgtggacg | gctggaagga | gctggccaac | 300 |
| tacgacctga | agctgtggag | ccagaacaag | aagagcctca | tcagggactg | gggcgaggcc | 360 |
| gtgttcgaca | tcttcgacaa | ggacggcagc | ggcagcatca | gcctggatga | gtggaaggcc | 420 |
| tactgcagaa | tcagcggcat | ctgcagcagc | gacgaggacg | ccgaaaagac | cttcaagcac | 480 |
| tgcgacctgg | acaacagcgg | caagctggac | gtggacgaga | tgaccagaca | gcacctgggc | 540 |
| ttctggtaca | ccctggaccc | caacgccgac | ggcctgtacg | gcaacttcgt | gccttgataa | 600 |

&lt;210&gt; 17

&lt;211&gt; 600

&lt;212&gt; DNA

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; Clytin mutant: 3C12 mutant\_dna

&lt;400&gt; 17

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| atggccgaca | ccgccagcaa | gtacgccgtg | aagctgaggc | ccaacttcga | caacoccaag | 60  |
| tgggtgaacc | ggcacaagtt | catgttcaac | ttcctggaca | tcaacggcga | cggcaagatc | 120 |
| accctggacg | agatcgtgag | caaggccagc | gacgacgtct | gcgccaagct | gggcgccacc | 180 |
| cccgagcaga | ccaagagaca | ccaggacgcc | gtggaggcct | tcttcaagaa | gatcggcatg | 240 |
| gactacggca | aggaggtgga | gttccccgcc | ttcgtggacg | gctggaagga | gctggccaac | 300 |
| tacgacctga | agctgtggag | ccaaaacaag | aagagcctca | tcagggactg | gggcgaggcc | 360 |
| gtgttcgaca | tcttcgacaa | ggacggcagc | ggcagcatca | gcctggacga | gtggaaggcc | 420 |
| tacggcagaa | tcagcggcat | ctgcagaagc | gacgaggacg | ccgaaaagac | cttcaagcac | 480 |



16

tgcgacctgg acaacagcgg caagctggac gtggacgaga tgaccagaca gcacctgggc 540  
ttctggtaca cectggaccc caacgccgac ggctgtacg gcaacttcgt gcttgataa 600

&lt;210&gt; 18

&lt;211&gt; 600

&lt;212&gt; DNA

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; Clytin mutant: 6H22 mutant\_dna

&lt;400&gt; 18

atggccgaca cggccagcaa gtacgccgtg aagctgaggc ccaacttcga caacccaag 60  
tgggtgaacc ggcacaagtt catgttcaac ttcttgga tcaacggcga cggcaaggtc 120  
accctggacg agatcgtgag caaggccagc gacgacatct gcgccaggct gggcgccacc 180  
cccgagcaga ccaagagaca ccaggacgcc gtggaggcct tcttcaagaa gatcggcatg 240  
gactacggca aagaggtgga gttccccgcc ttctgtgacg gctggaagga gctggccaac 300  
tacgacctga agctgtggag ccagaacaag aagagcctca tcagggactg gggcgaggcc 360  
gtgttcgaca ttttcgacaa ggacggcagc ggcagcatca gcctggatga gtggaaggcc 420  
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ttctggtaca cectggaccc caacgccgac ggctgtacg gcaacttcgt gcttgataa 600

&lt;210&gt; 19

&lt;211&gt; 597

&lt;212&gt; DNA

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; Clytin mutant: 12mutCly\_dna

&lt;400&gt; 19

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tgggtgaacc ggcacaagtt catgttcaac ttcttgga tcaacggcga cggcaagatc 120



17

accctggacg agatcgtgag caaggccagc gacgacatct ggcccaagct ggaggccacc 180  
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&lt;210&gt; 20

&lt;211&gt; 32

&lt;212&gt; DNA

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; synthetic primer

&lt;400&gt; 20

gatgacgacg acaagatggc cgacaccgcc ag

32

&lt;210&gt; 21

&lt;211&gt; 33

&lt;212&gt; DNA

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; synthetic primer

&lt;400&gt; 21

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33

&lt;210&gt; 22

&lt;211&gt; 33

&lt;212&gt; DNA

&lt;213&gt; Unknown

18

&lt;220&gt;

&lt;223&gt; synthetic primer

&lt;400&gt; 22

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33

&lt;210&gt; 23

&lt;211&gt; 27

&lt;212&gt; DNA

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; synthetic primer

&lt;400&gt; 23

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27

&lt;210&gt; 24

&lt;211&gt; 99

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 24

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60

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99